E. Saoud

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

Does Not Comply
Corrected Diskette Needed

pp 1-3

3 <110> APPLICANT: Walker, Ameae M.
5 <120> TITLE OF INVENTION: PROLACTIN ANTAGONISTS AND USES THEREOF
7 <130> FILE REFERENCE: Walker_2500_097US2
9 <140> CURRENT APPLICATION NUMBER: 09/065,330B
10 <141> CURRENT FILING DATE: 1998-04-23
12 <150> PRIOR APPLICATION NUMBER: PCT/US97/01435
13 <151> PRIOR FILING DATE: 1997-01-30
15 <150> PRIOR APPLICATION NUMBER: 08/594,809
16 <151> PRIOR FILING DATE: 1996-01-31
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 832
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: mutation
29 <222> LOCATION: (622)..(624)
30 <223> OTHER INFORMATION: This is the codon for the substituted amino acids
31 of the mutated sequence.
33 <400> SEQUENCE: 1
34 aacatgaaca tcaaaggatc gccatggaaa gggtccctcc tgctgctgct ggtgtcaaac 60
35 ctgctgctgt gccagagcgt ggccccttg cccatctgtc ccggcggggc tgcccgatgc 120
36 caggtgaccc ttcgagacct gtttgaccgc gccgtcgtcc tgtcccacta catccataac 180
37 ctctcctcag aaatgttcag cgaattcgat aaacggtata cccatggccg ggggttcatt 240
38 accaaggcca tcaacagctg ccacacttct tcccttgcca cccccgaaga caaggagcaa 300
39 gcccaacaga tgaatcaaaa agactttctg agcctgatag tcagcatatt gcgatcctgg 360
40 aatgagcctc tgtatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420
41 atcctatcca aagctgtaga gattgaggag caaaccaaac ggcttctaga gggcatggag 480
42 ctgatagtca gccaggttca tcctgaaacc aaagaaaatg agatctaccc tgtctggtcg 540
43 ggacttccat ccctgcagat ggctgatgaa gagtctcgcc tttctgctta ttataaccctg 600
OK 44 **ctccactgcc tacgcaggga tnnncataaa atcgacaatt atctcaagct cctgaagtgc 660**
45 cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatctattt ctgagaaggt 720
46 ccttaatgat ccgttccatt gcaagcttct tttagttgta tctcttttga atccatgctt 780
47 gggtgtaaca ggtctcctct taaaaaataa aaactgactc gttagagaca tc 832
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 228
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <220> FEATURE:
57 <221> NAME/KEY: VARIANT
58 <222> LOCATION: (208)
59 <223> OTHER INFORMATION: Site mutated codon where the normal codon coding
60 for serine is modified preferably to encode for
61 aspartate or glutamate, most preferably aspartate.
63 <400> SEQUENCE: 2
64 Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu

? a codon consists of three bases

RAW SEQUENCE LISTING DATE: 06/05/2000
PATENT APPLICATION: US/09/065,330B TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

```
65   1               5                  10                  15
67 Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
68                  20                  25                  30
70 Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
71          35                  40                  45
73 Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
74      50                  55                  60
76 Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
77  65                  70                  75                  80
79 Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
80                  85                  90                  95
82 Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
83              100                 105                 110
85 Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
86          115                 120                 125
88 Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
89      130                 135                 140
91 Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
92 145                 150                 155                 160
94 Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
95                  165                 170                 175
97 Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
98              180                 185                 190
W--> 101 Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
102          195                 200                 205
104 His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
105     210                 215                 220
107 Asn Asn Asn Cys
108 225
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 23
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
119       is a primer.
121 <400> SEQUENCE: 3                                                    23
122 gcagggatga ccacaaggtt gac
125 <210> SEQ ID NO: 4
126 <211> LENGTH: 24
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
132       is a primer.
134 <220> FEATURE:
135 <221> NAME/KEY: variation
136 <222> LOCATION: (12)
137 <223> OTHER INFORMATION: This is a codon that can be replaced for nucleic
```

a codon consists of three bases — location 12 "n" is only one

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

138 acid substitutes.
140 <400> SEQUENCE: 4 24
W--> 141 cgcaagggat gnacacaagg ttga
144 <210> SEQ ID NO: 5
145 <211> LENGTH: 22
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
153 is a primer.
155 <220> FEATURE:
156 <221> NAME/KEY: variation
157 <222> LOCATION: (12)
158 <223> OTHER INFORMATION: This is a codon that can be replaced for nucleic
159 acid substitutes.
161 <400> SEQUENCE: 5 22
W--> 162 acgcagggat gnkataaaat cg
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 26
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
172 is a primer.
174 <400> SEQUENCE: 6 26
175 cgtggccccc atatgttgcc catctg
W--> 178 4

same error

delete at end of file

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:13

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6